

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
 5 (A) NAME: Federal Republic of Germany, ultimately represented by the Director of the Robert-Koch-Institut
 (B) STREET: Nordufer 20
 (C) CITY: Berlin
 10 (D) STATE OR PROVINCE: Berlin
 (E) COUNTRY: Germany
 (F) POSTAL CODE: 13353

15 (ii) TITLE OF INVENTION: Costimulating polypeptide of T cells, monoclonal antibodies, and the preparation and use thereof

(iii) NUMBER OF SEQUENCES: 4

20 (iv) COMPUTER-READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

25 (v) CURRENT APPLICATION DATA:
 APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO: 1:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2641 base pairs
 (B) TYPE: Nucleotides
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGAGAGCCTG AATTCAGTGT CAGCTTTGAA CACTGAACGC GAGGACTGTT AACTGTTTCT	60
GGCAAACATG AAGTCAGGCC TCTGGTATTT CTTTCTCTTC TGCTTGCGCA TTAAAGTTTT	120
AACAGGAGAA ATCAATGGTT CTGCCAATTA TGAGATGTTT ATATTTCAAC ACGGAGGTGT	180
ACAAATTTTA TGCAAATATC CTGACATTGT CCAGCAATTT AAAATGCAGT TGCTGAAAGG	240
GGGGCAAATA CTCTGCGATC TACTAAGAC AAAAGGAAGT GGAAACACAG TGTCCATTAA	300
GAGTCTGAAA TTCTGCCATT CTCAGTTATC CAACAACAGT GTCTCTTTTT TTCTATACAA	360
CTTGGACCAT TCTCATGCCA ACTATTACTT CTGCAACCTA TCAATTTTTG ATCCTCCTCC	420
TTTTAAAGTA ACTCTTACAG GAGGATATTT GCATATTTAT GAATCACAAC TTTGTTGCCA	480
GCTGAAGTTC TGGTTACCCA TAGGATGTGC AGCCTTTGTT GTAGTCTGCA TTTGGGATG	540
CATACTTATT TGTTGGCTTA CAAAAAGAA GTATTCATCC AGTGTGCACG ACCCTAACGG	600

TGAATACATG TTCATGAGAG CAGTGAACAC AGCCAAAAA TCTAGACTCA CAGATGTGAC	660
CCTATAATAT GGAAGTCTGG CACCCAGGCA TGAAGCACGT TGGCCAGTTT TCCTCAACTT	720
GAAGTGCAAG ATTCTCTTAT TTCCGGGACC ACGGAGAGTC TGACTTAACT ACATACATCT	780
TCTGCTGGTG TTTGTTCAT TCTGGAAGAA TGACTGTATC AGTCAATGGG GATTTTAAAC	840
GACTGCCTTG GTACTGCCGA GTCCTCTCAA AACAAACACC CTCTTGCAAC CAGCTTTGGA	900
GAAAGCCCAG CTCCTGTGTG CTCCTGGGA GTGGAATCCC TGTCTCCACA TCTGCTCCTA	960
GCAGTGCATC AGCCAGTAAA ACAAACACAT TTACAAGAAA AATGTTTTAA AGATGCCAGG	1020
GGTACTGAAT CTGCAAAGCA AATGAGCAGC CAAGGACCAG CATCTGTCCG CATTCTACTA	1080
TCATACTACC TCTTCTTTCT CTAGGGATGA GAATTCCTCT TTTAATCAGT CAAGGGAGAT	1140
GCTTCAAAGC TGGAGCTATT TTATTTCTGA GATGTTGATG TGAAGTGTAC ATTAGTACAT	1200
ACTCAGTACT CTCCTTCAAT TGCTGAACCC CAGTTGACCA TTTTACCAAG ACTTTAGATG	1260
CTTTCTTGIG CCCTCAATTT TCTTTTTTAA AATACTTCTA CATGACTGCT TGACAGCCCA	1320
ACAGCCACTC TCAATAGAGA GCTATGTCTT ACATTCTTTC CTCTGCTGCT CAATAGTTTT	1380
ATATATCTAT GCATACATAT ATACACACAT ATGATATATAA AATTCATAAT GAATATATTT	1440
GCCTATATTC TCCCTACAAG AATATTTTTG CTCCAGAAAG ACATGTTCTT TTCTCAAATT	1500
CAGTTAAAAT GGTTTACTTT GTTCAAGTTA GTGGTAGCAA ACATTGCCCC GAATTGAAAG	1560
CAAATTTATT TTATTATCCT ATTTTCTACC ATTATCTATG TTTTCATGGT GCTATTAATT	1620
ACAAGTTTAG TTCTTTTTGT AGATCATATT AAAATTGCAA AAAAAATCAT CTTTAATGGG	1680
CCAGCATTCT CATGGGGTAG AGCAGAATAT TCATTTAGCC TGAAGGCTGC AGTTACTATA	1740
GGTTGCTGTC AGACTATACC CATGGTGCCT CTGGGCTTGA CAGGTCAAAA TGGTCCCCAT	1800
CAGCCTGGAG CAGCCCTCCA GACCTGGGTG GAATTCAGG GTTGAGAGAC TCCCCTGAGC	1860
CAGAGGCCAC TAGGTATTCT TGCTCCAGA GGCTGAAGTC ACCCTGGGAA TCACAGTGGT	1920
CTACCTGCAT TCATAATTCC AGGATCTGTG AAGAGCACAT ATGTGTCAGG GCACAATTCC	1980
CTCTCATAAA AACCACACAG CCTGGAAATT GGCCCTGGCC CTTCAAGATA GCCTTCTTTA	2040
GAATATGATT TGGCTAGAAA GATTCTTAAA TATGTGGAAT ATGATTATTC TTAGCTGCAA	2100
TATTTTCTCT ACTTCCTGTC TGCATGCCCA AGGCTTCTGA AGCAGCCAAT GTCGATGCAA	2160
CAACATTTGT AACTTTAGGT AAAGTGGGAT TATGTTGTAG TTTAACATTT TGTAAGTGTG	2220
TGCTTATAGT TTACAAGTGA GACCCGATAT GTCATTATGC ATACTTATAT TATCTTAAGC	2280
ATGTGTAATG CTGGATGTGT ACAGTACAGT ACTGAACTTG TAATTTGAAT CTAGTATGGT	2340
GTCTGTTTTT CAGCTGACTT GGACAACCTG ACTGGCTTTG CACAGGTGTT CCCTGAGTTG	2400
TTTGACAGTT TCTGTGTGTG GGGTGGGGTA TGGGGAGGAG AACCTTCATG GTGGCCACC	2460
TGGCCTGGTT GTCCAAGCTG TGCCTCGACA CATCCTCATC CCCAGCATGG GACACCTCAA	2520

GATGAATAAT AATTCACAAA ATTTCTGTGA AATCAAATCC AGTTTAAAGA GGAGCCACTT 2580
ATCAAAGAGA TTTTAACAGT AGTAAGAAGG CAAAGAATAA ACATTGATA TTCAGCAACT 2640
G 2641

(2) INFORMATION FOR SEQ ID NO: 2:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 amino acids
(B) TYPE: Amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190
Arg Leu Thr Asp Val Thr Leu
195

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleotides

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: Yes

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

MGNCTSACNG AYG TNAC

17

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleotides

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: Yes

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

MGNYTDACNG AYG TNAC

17